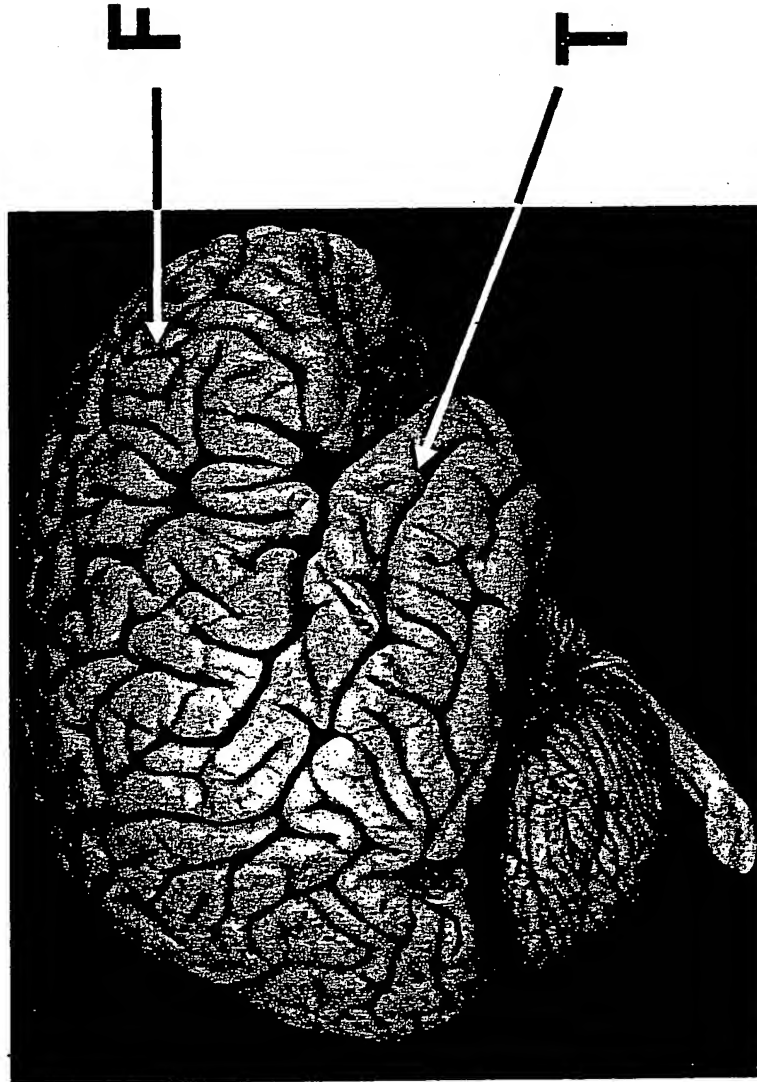


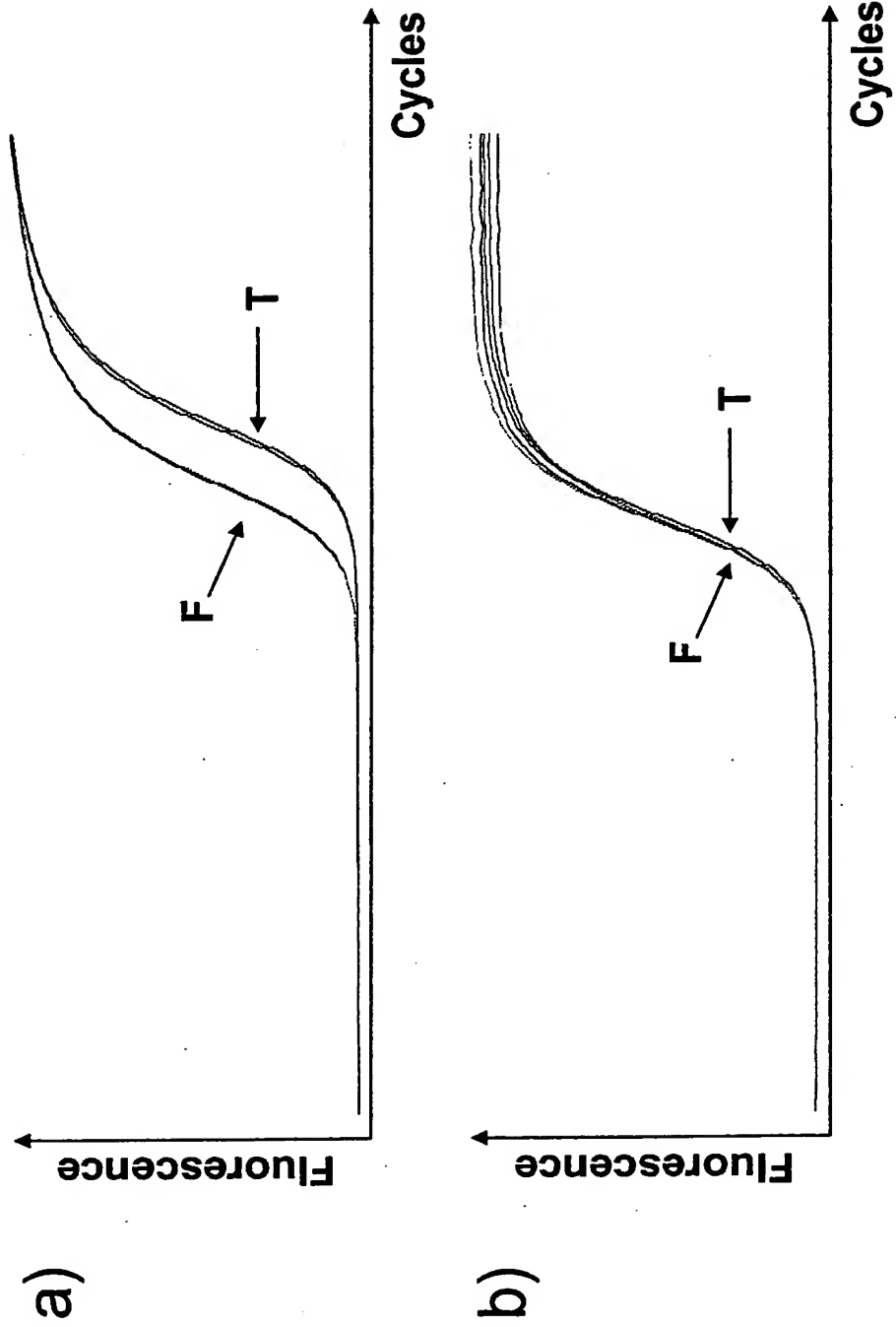
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**Fig. 1: Identification of Genes Involved
in Alzheimer's Disease Pathology**



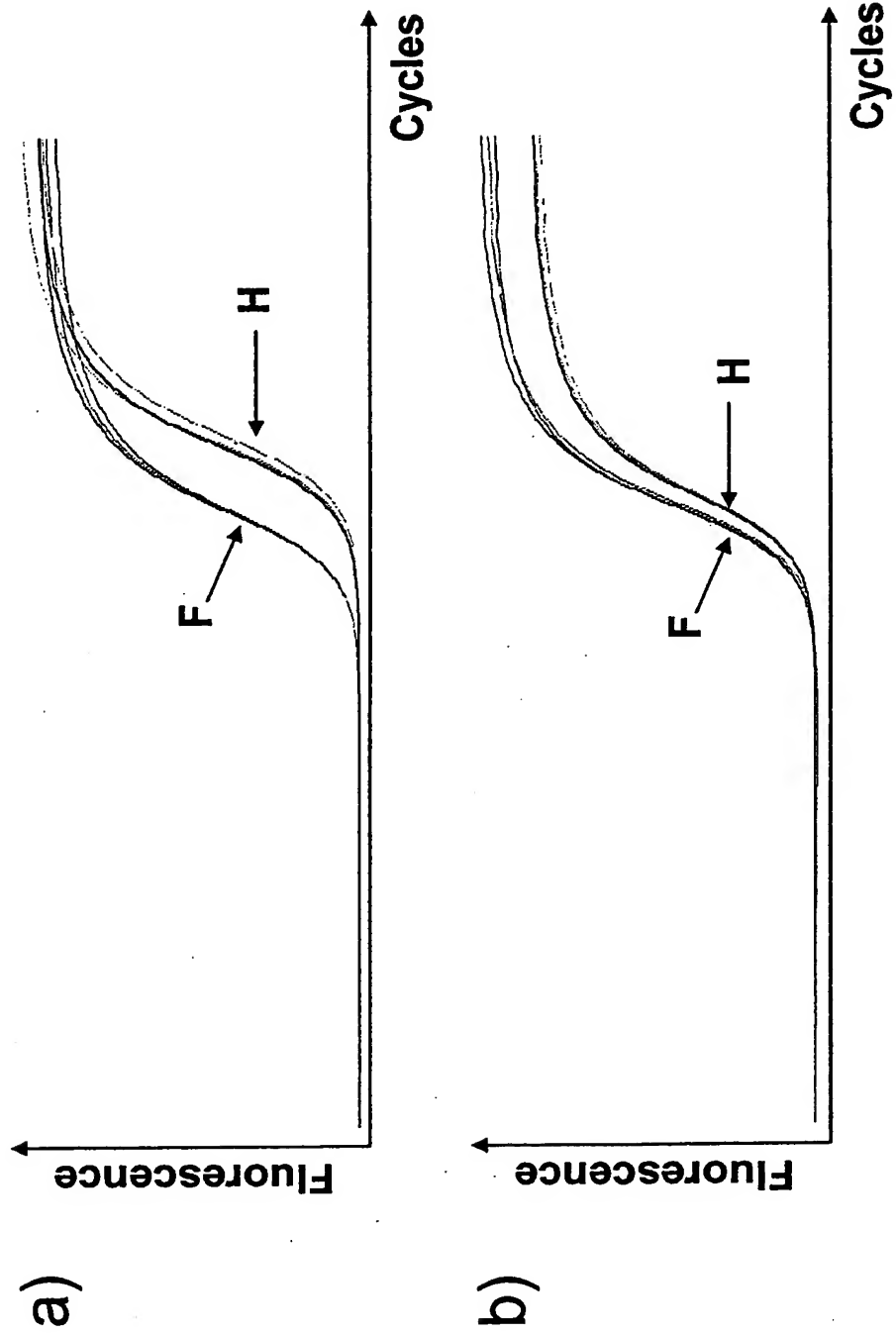
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Fig. 2: Verification of differential expression of human TARPP by quantitative RT-PCR



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Fig. 3: Verification of differential expression of human TARPP by quantitative RT-PCR



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Fig. 4 : SEQ ID NO. 1: amino acid sequence of human TARPP protein**Length: 813 aa**

1 MSEQGDNLQA IAEEGGTEQE TATPENGIVK SESLDEEEKL ELQRRLEAQN
51 QERRKSKSGA GKGKLTRSLA VCEESSARPG GESLQDQESI HLQLSSFSSSL
101 QEEDKSRKDD SEREKEKDKN KDKTSEKPKI RMLSKDCSQE YTDSTGIDLH
151 EFLINTLKNN SRDRMILLKM EQEIIDFIAD NNNHYKKFPQ MSSYQRMLVH
201 RVAAYFGLDH NVDQTGKSVI INKTSSTRIP EQRFCHELKD EKGEESQKRF
251 ILKRDNSSID KEDNQSVCSQ ESLFVENSRL LEDSNICNET YKKRQLFRGN
301 RDGSGRTSGS RQSSSENELK WSDHQRAWSS TSDSSNRNL KPAMTKTASF
351 GGITVLTRGD STSSTRSTGK LSKAGSESSS SAGSSGSLSR THPPLQSTPL
401 VSGVAAGSPG CVPYPENGIG GQVAPSSTSY ILLPLEAATG IPPGSILLNP
451 HTGQPFVNPDP GTPAIYNPPT SQQPLRSAMV GQSQQQPPQQ QPSPQPQQQV
501 QPPQPQMAGP LVTQSVQGLQ ASSQSVQYPA VSFPPQHLLP VSPTQHFPMPR
551 DDVATQFGQM TLRQSSGET PEPPSGPVYP SSLMPQPAQQ PSYVIASGQ
601 QLPTGGFSGS GPPISQQVLQ PPPSPQGFVQ QPPPAQMPVY YYPSGQYPTS
651 TTQQYRPMAP VQYNAQRSQQ MPQAAQQAGY QPVLSGQQGF QGLIGVQQPP
701 QSQNVINNQQ GTPVQSVMVY YPTMSSYQVP MTQGSQGLPQ QSYQQPIMLP
751 NQAGQGSLPA TGMPVYCNVT PPTPQNNLRL IGPHCPSSTV PVMSASCRTN
801 CASMSNAGWQ VKF*

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**Fig. 5: Alignment of SEQ ID NO. 1human
TARPP, with mouse TARPP**

Length: 813 aa

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1  MSEQGDNLNQAIAEEGGTEQETATPENGIVKSESLDEEEKLELQRRLEAQN 50
   ||||| | | ||| | | . | ||||| . ||||| ||||| ||||| |||||
1  MSEQGGLTPTILEEGQTEPESA . PENGILKSESLDEEEKLELQRRLAAQN 49

51  QERRKSKSGAGKGKLTRSLAVCEESSARPGGESLQDQESIHLQLSSFSSL 100
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
50  QERRKSKSGAGKGKLTRSLAVCEESSARSGGESHQDQESIHLQLSSFPSL 99

101  QEEDKSRKDDSEREKEKDKNKDKTSEKPKIRMLSKDCSQEYTDSTGIDLH 150
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
100  QEEDKSRKDDSEREKEKDKNREKLSEKPKIRMLSKDCSQEYTDSTGIDLH 149

151  EFLINTLKNNSRDRMILLKMEQEIIDFIADNNNHKKFPQMSSYQRMVLVH 200
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
150  GFLINTLKNNSRDRMILLKMEQEMIDFIADSNNHKKFPQMSSYQRMVLVH 199

201  RVAAYFGLDHNVDQTGKSVIINKTSSTRIPEQRFCEHLKDEKGEESQKRF 250
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
200  RVAAYFGLDHNVDQTGKSVIINKTSSTRIPEQRFCEHLKDEKSEESQKRF 249

251  ILKRDNSSIDKEDNQ.....SV 267
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
250  ILKRDNSSIDKEDNQNRMHPPFRDDRRSKSIEEEEEYQVRERIFAHDSV 299

268  CSQESLFVENSRLLEDNICNETYKKRQLFRGNRDGSGRTSGSRQSSSEN 317
     ||||| ||||| .: ||||| || || ||||| ||||| ||||| ||||| |||||
300  CSQESLFLDNSRLQEDMHICNETYKKRQLFRAHRDSSGRTSGSRQSSSET 349

318  ELKWSDHQRAWSSSTDSDSSNRNLKPAMTKTASFGGITVLTRGDSTSSTRS 367
     ||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
350  ELRWPDHQRAWSSSTDSDSSNRNLKPMTTKTASFGGITVLTRGDSTSSTRS 399

368  TGKLSKAGSESSSSAGSSGSLSRTHPPLQSTPLVSGVAAGSPGCVYPYEN 417
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
400  AGKLSKTGSESSSSAGSSGSLSRTHP..QSTALTSSVAAGSPGCMAYSEN 447

418  GIGGQVAPSSTSYILLPLEAATGIPPGSILLNPHTGQPFVNPDPGTPAIYN 467
     |. ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
448  GMGGQVPPSSTSYILLPLESATGIPPGSILLNPHTGQPFVNPDPGTPAIYN 497

468  PPTSQQPLRSAMVGQSQQQPPQQQSPQPPQQQVQPPQPMAGPLVTQSVQ 517
     || ||||| || | || ||||| ||||| ||||| ||||| ||||| |||||
498  PPGSQQTLRGTVGGQ . PQQPPQQQSPQPPQQQVQASQPMAGPLVTQ... 543

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518 GLQASSQSVQYPAVSFPPQHLLPVSPQHFPMRDDVATQFGQMTLSRQSS 567
      |:::| || |:::|||||
544 .....REELAAQFSQLSMSRQSS 561

568 GETPEPPSGPVYPSSLMPQPAQQPSYVIASTGQQLPTGGFSGSGPPISQQ 617
      |:||||| |||.||:| || |||| | |||| | |||||
562 GDTPEPPSGTVYPASLLPQTAQPQSYVITSAGQQLSTGGFSDSGPPISQQ 611

618 VLQPPPSPOGFVQQPPPAQMPVYYYPSGQYPTSTTQQYRPMAPVQYNAQR 667
      ||| ||||| ||||| ||||| ||||| |||||.|||:| |||.|||
612 VLQAPPSPOGFVQQPPPAQMSVYYYPSGQYPTSTSQQYRPLASVQYSAQR 661

668 SQQMPQAAQQAGYQPVLSGQQGFQGLIGVQQPPQSQNVINNQQGTPVQSV 717
      |||.|| | ||||| ||||| |||||:|.||| || |...||| || |
662 SQQIPQTTQQAGYQPVLSGQQGFQGMGVQQSAHSQGVMSQQGAPVHGV 711

718 MVSYPMTSSYQVPMTQGSQGLPQQSYQQPIMLPNQAGQGSLPATGMPVYC 767
      ||||| ||||| ||||| |||||.|||.|| | |||||.||| |||||
712 MVSYPMTSSYQVPMTQGSQAVPQQTYQQPIMLPNQAGQGSLPATGMPVYC 761

768 NVTPTTPQNNLRLIGPHCPSSSTVPVMSASCRTNCASMSNAGWQVKF 813
      ||||| ||||| ||||| ||||| ||||| |||||.||| |||||
762 NVTPPNPQNNLRLMGPHCPSSSTVPVMSASCRTNCGNVSNAGWQVKF 807

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Fig. 6: SEQ ID NO. 2: nucleotide sequence of human TARPP coding sequence

Length: 2442 bp

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1  ATGTCTGAGC AAGGAGACCT GAATCAGGCA ATAGCAGAGG AAGGAGGGAC
51  TGAGCAGGAG ACGGCCACTC CAGAGAACGG CATTGTTAAA TCAGAAAGTC
101 TGGATGAAGA GGAGAAACTG GAACTGCAGA GGCGGCTGGA GGCTCAGAAT
151 CAAGAAAGAA GAAAATCCAA GTCAGGAGCA GGAAAAGGTA AACTGACTCG
201 CAGYCTTGCT GTCTGTGAGG AATCTTCTGC CAGACCAGGA GGTGAAAGTC
251 TTCAGGATCA GGAATCAATT CATTACAGC TTTCCAGTTT TTCCAGCCTG
301 CAAGAGGAGG ATAAATCTAG GAAAGATGAC TCTGAAAGAG AAAAAGAAAA
351 GGATAAAAAA AAAGATAAAA CCTCTGAAAA ACCCAAGATC AGAATGTTAT
401 CAAAAGATTG CAGCCAAGAA TACACGGATT CTACAGGCAT AGACTTACAC
451 GAGTTTCTGA TTAACACATT AAAGAATAAT TCCAGGGACA GGATGATACT
501 TTTGAAATG GAGCAGGAAA TTATTGATTT CATTGCTGAC AACATAATC
551 ATTATAAAAA GTTCCCTCAG ATGTCATCGT ATCAGAGGAT GCTTGTCCAT
601 CGAGTGGCAG CTTATTTTGG ATTGGATCAC AATGTGGATC AAACAGGAAA
651 ATCTGTTATC ATCAACAAGA CCAGCAGCAC CAGAATACCA GAGCAAAGGT
701 TTTGTGAACA TTTAAAAGAT GAAAAAGGTG AAGAATCCCA GAAGCGGTTT
751 ATCTTGAAGC GAGATAACTC TAGTATTGAT AAAGAAGACA ATCAGTCAGT
801 TTGCTCCCG GAAAGCCTTT TTGTGGAAAA CAGTAGGCTC TTGGAAGACA
851 GTAACATATG CAATGAGACC TATAAGAAAA GACAGCTCTT TCGGGGCAAC
901 AGAGATGGCT CAGGGAGAAC ATCTGGGAGT CGACAGAGCA GCTCAGAAAA
951 TGAACTCAAG TGGTCTGACC ACCAAAGGGC CTGGAGCAGC ACAGACTCCG
1001 ACAGTTCCAA CCGCAATCTA AAGCCCGCCA TGACCAAGAC GGCGAGTTTT
1051 GGGGGCATCA CGGTGCTGAC CAGGGGTGAC AGCACTTCCA GTAGTAGGAG
1101 TACCGGGAAG CTGTCCAAAG CAGGTTCCGA GTCTTCCAGC AGTGCAGGCT
1151 CCTCAGGATC GCTGTCCCGC ACCCATCCAC CTCTCCAGAG CACACCCCTA
1201 GTCTCAGGTG TGGCAGCTGG CTCTCCAGGC TGTGTGCCTT ATCCAGAGAA
1251 TGGAATAGGG GGCCAGGTTG CTCCCAGCAG CACCAGCTAC ATCCTCCTTC
1301 CACTTGAAGC TGCAACAGGC ATCCCGCCTG GAAGCATCCT TCTTAATCCA
1351 CACACAGGCC AGCCCTTTGT GAATCCCGAT GGAACTCCTG CAATATACAA
1401 CCCACCCACC AGTCAGCAGC CCCTGCGAAG CGCCATGGTG GGGCAGTCCC
1451 AACAGCAGCC GCCACAGCAG CAGCCCTCCC CGCAGCCCCA ACAGCAGGTC
1501 CAGCCACCGC AGCCACAGAT GGCAGGCCCT CTGGTCACTC AGTCTGTCCA
1551 GGGGCTGCAG GCTTCCTCCC AGTCAGTGCA ATATCCGGCA GTCTCTTTTC
1601 CTCCCCAGCA CCTCCTACCT GTGTCTCCAA CGCAGCACTT TCCCATGAGA
1651 GATGATGTGG CAACACAGTT TGGCCAGATG ACCCTGAGCC GGCAGTCCTC
1701 GGGGGAGACT CCTGAACCCC CATCAGGTCC TGTCTACCCA TCCTCCCTTA
1751 TGCCACAGCC GGCCCAGCAG CCCAGCTATG TAATCGCCTC TACAGGCCAG
1801 CAGCTTCCTA CAGGAGGATT CTCAGGCTCT GGCCCTCCCA TCTCCAGCA
1851 GGTCTCTCAG CCCCCTCCCT CACCACAGGG ATTCGTGCAA CAGCCTCCGC
1901 CTGCACAGAT GCCTGTATAT TATTACCCAT CTGGTCAGTA CCCTACCTCA
1951 ACCACGCAAC AGTACCGGCC CATGGCCCCG GTTCAGTACA ACGCTCAGAG
2001 GAGTCAACAG ATGCCACAGG CAGCACAGCA AGCAGGTTAC CAGCCAGTCT
2051 TGTCTGGTCA ACAGGGATTG CAAGGCCTAA TAGGAGTGCA GCAGCCACCT
2101 CAGAGTCAGA ACGTGATAAA TAACCAACAA GGAACTCCGG TGCAAAGCGT
2151 GATGGTTTCC TACCCAACAA TGTCTTCTTA TCAGGTGCCA ATGACCCAGG
2201 GTTCTCAAGG ACTGCCCCAG CAGTCATACC AACAGCCAAT CATGTACCT
2251 AATCCAGCAG GTCAAGGGTC ACTCCCAGCC ACTGGAATGC CTGTTACTG
2301 TAATGTCACA CCGCCCACCC CTCAGAACAA CCTTAGGCTG ATTGGCCCAC
2351 ACTGCCCTC CAGCACTGTC CCAGTGATGT CAGCTAGCTG CAGAACAAC
2401 TGTGCAAGTA TGAGCAATGC TGGTTGGCAG GTCAAATTCT GA

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Fig. 7: SEQ ID NO. 3: nucleotide sequence of human TARPP cDNA

Length: 3212 bp

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1  GTGATTTGCT GGAAGCTGGT CATTAGTGTT GACGATGTGT CACACTGTGT
51  AAGGGAATCG CATGGAGATG GGCATTCCGA ACTGTTAATG GGGACATGGG
101 ACTCCAGTTG TCTCTGATCA CTTGTGTGGA TTTTCCTGGC GTAGAACGAC
151 AGAAGCCGCT AGTAAGTCGC CAAGACCTAC AGCAGGAATT CTGCACCAAA
201 GGGCATAAAA TCTTGTTATT TTAATTGCA TCTGGGAGAA TGTCTGAGCA
251 AGGAGACCTG AATCAGGCAA TAGCAGAGGA AGGAGGGACT GAGCAGGAGA
301 CGGCCACTCC AGAGAACGGC ATTGTTAAAT CAGAAAGTCT GGATGAAGAG
351 GAGAACTGG AACTGCAGAG GCGGCTGGAG GCTCAGAATC AAGAAAGAAG
401 AAAATCCAAG TCAGGAGCAG GAAAAGGTAA ACTGACTCGC AGYCTTGCTG
451 TCTGTGAGGA ATCTTCTGCC AGACCAGGAG GTGAAAGTCT TCAGGATCAG
501 GAATCAATTC ATTTACAGCT TTCCAGTTTT TCCAGCCTGC AAGAGGAGGA
551 TAAATCTAGG AAAGATGACT CTGAAAGAGA AAAAGAAAAG GATAAAAACA
601 AAGATAAAAC CTCTGAAAAA CCCAAGATCA GAATGTTATC AAAAGATTGC
651 AGCCAAGAAT ACACGGATTC TACAGGCATA GACTTACACG AGTTTCTGAT
701 TAACACATTA AAGAATAATT CCAGGGACAG GATGATACTT TTGAAAATGG
751 AGCAGGAAAT TATTGATTTC ATTGCTGACA ACAATAATCA TTATAAAAAG
801 TTCCCTCAGA TGTCATCGTA TCAGAGGATG CTTGTCCATC GAGTGGCAGC
851 TTATTTTGGG TTGGATCACA ATGTGGATCA AACAGGAAAA TCTGTTATCA
901 TCAACAAGAC CAGCAGCACC AGAATACCAG AGCAAAGGTT TTGTGAACAT
951 TTAAAAGATG AAAAAGGTGA AGAATCCCAG AAGCGGTTTA TCTTGAAGCG
1001 AGATAACTCT AGTATTGATA AAGAAGACAA TCAGTCAGTT TGCTCCCAGG
1051 AAAGCCTTTT TGTGGAAAAA AGTAGGCTCT TGGAAGACAG TAACATATGC
1101 AATGAGACCT ATAAGAAAAG ACAGCTCTTT CGGGGCAACA GAGATGGCTC
1151 AGGGAGAACA TCTGGGAGTC GACAGAGCAG CTCAGAAAAT GAACTCAAGT
1201 GGTCTGACCA CCAAAGGGCC TGGAGCAGCA CAGACTCCGA CAGTTCCAAC
1251 CGCAATCTAA AGCCCGCCAT GACCAAGACG GCGAGTTTTG GGGGCATCAC
1301 GGTGCTGACC AGGGGTGACA GCACTTCCAG TACTAGGAGT ACCGGGAAGC
1351 TGTCCAAAGC AGGTTCCGAG TCTTCCAGCA GTGCAGGCTC CTCAGGATCG
1401 CTGTCCCACA CCCATCCACC TCTCCAGAGC ACACCCCTAG TCTCAGGTGT
1451 GGCAGCTGGC TCTCCAGGCT GTGTGCCTTA TCCAGAGAAT GGAATAGGGG
1501 GCCAGGTTGC TCCCAGCAGC ACCAGCTACA TCCTCCTTCC ACTTGAAGCT
1551 GCAACAGGCA TCCCGCCTGG AAGCATCCTT CTTAATCCAC ACACAGGCCA
1601 GCCCTTTGTG AATCCCGATG GAACTCCTGC AATATACAAC CCACCCACCA
1651 GTCAGCAGCC CCTGCGAAGC GCCATGGTGG GGCAGTCCCA ACAGCAGCCG
1701 CCACAGCAGC AGCCCTCCCC GCAGCCCCAA CAGCAGGTCC AGCCACCGCA
1751 GCCACAGATG GCAGGCCCTC TGGTCACTCA GTCTGTCCAG GGGCTGCAGG
1801 CTCCTCCCA GTCAAGTCAA TATCCGGCAG TCTCTTTTCC TCCCAGCAC
1851 CTCCTACCTG TGTCTCCAAC GCAGCACTTT CCCATGAGAG ATGATGTGGC
1901 AACACAGTTT GGCCAGATGA CCCTGAGCCG GCAGTCCTCG GGGGAGACTC
1951 CTGAACCCCC ATCAGGTCCT GTCTACCCAT CCTCCCTTAT GCCACAGCCG
2001 GCCCAGCAGC CCAGCTATGT AATCGCCTCT ACAGGCCAGC AGCTTCCTAC
2051 AGGAGGATT CAGGCTCTG GCCCTCCCAT CTCCCAGCAG GTCCTCCAGC
2101 CCCCTCCCTC ACCACAGGGA TTCGTGCAAC AGCCTCCGCC TGCACAGATG
2151 CCTGTATATT ATTACCCATC TGGTCAGTAC CCTACCTCAA CCACGCAACA
2201 GTACCGGCCC ATGGCCCCGG TTCAGTACAA CGCTCAGAGG AGTCAACAGA
2251 TGCCACAGGC AGCACAGCAA GCAGGTTACC AGCCAGTCTT GTCTGGTCAA
2301 CAGGGATTCC AAGGCCTAAT AGGAGTGCAG CAGCCACCTC AGAGTCAGAA

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2351 CGTGATAAAT AACCAACAAG GAACTCCGGT GCAAAGCGTG ATGGTTTCCT
2401 ACCCAACAAT GTCTTCTTAT CAGGTGCCAA TGACCCAGGG TTCTCAAGGA
2451 CTGCCCCAGC AGTCATACCA ACAGCCAATC ATGCTACCTA ACCAGGCAGG
2501 TCAAGGGTCA CTCCCAGCCA CTGGAATGCC TGTTTACTGT AATGTCACAC
2551 CGCCCACCCC TCAGAACAAC CTTAGGCTGA TTGGCCCACA CTGCCCCCTCC
2601 AGCACTGTCC CAGTGATGTC AGCTAGCTGC AGAACAAACT GTGCAAGTAT
2651 GAGCAATGCT GGTGCGCAGG TCAAATTCTG AGAGCTCTGG CTGTGGTACA
2701 TTTCTTCAGA TATTTCTCAT GGCCTTTGAT GGAAGAGGAA CAAGGTGGGA
2751 AAAGTGGCTG AGGACTTAAG TATTCCTCA AACTCAAAT GATTGCTGCT
2801 GGTATTCTGT AAAAAGTAAA CAAAGACTAA TATACACGTT AGCTGGTTAA
2851 TGGTGATAT TTCTGTCATG TCTGCTAGGT ATGCCTTTAT AGCTTAGCTA
2901 GTGACATGAA TTCATCAAGG TAAGATTCTC TCCTACCACT GAATACCACT
2951 GTGTAGATTA TAATATCCCT AATTTGGATT AGTTTTGTAC TTTGTGTTGA
3001 GTTTGTGATG CTAAAAGTAT TTAAAAATTA TATACTAAAT CACATTGTAC
3051 CAAAGCTGTA ATGGAAAAGC AAAGAAGAAC TGATGAATTG AAGGAATAAT
3101 TTATATACAT TATAGAGTTT TCTTTTAA TGGATATATA CTGTATTGTA
3151 GTGTTTAATC AAAATAAAAC TATTTGACCT TATGGAGGAA GGTGATGTTT
3201 TTACCACTAA AA
```

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Fig. 8: SEQ ID NO. 4

Length: 69 bp

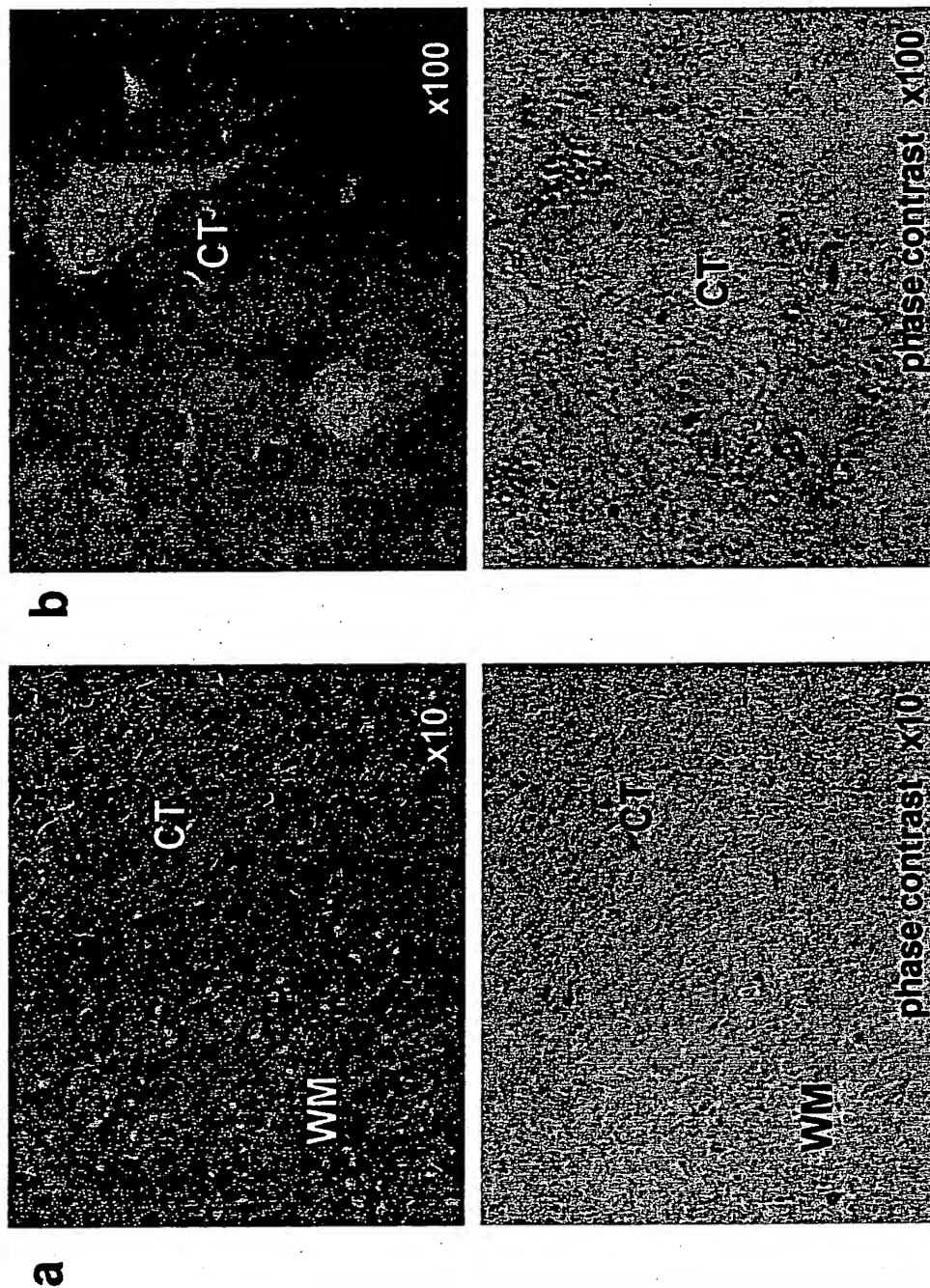
2471 ACAGCCAATCATGCTACCTAACCAGGCAGGTCAAGGGTCACTCCCAGCCA
CTGGAATGCCTGTTTACTG 2539

aw955967	+----->
bf439219	<-----+
z28447	+----->
w77929	+-----+
bg191076	v-----+>
bg201699	+----->
bg201698	+----->
bg391751	+----->
t06519	+----->
t66224	+----->
f12207	+----->
bi553063	+----->
m79028	+----->
aa425570	+----->
m86106	+----->
hsm80139	+----->
be671104	<-----+
aa733082	<-----+
r88588-2	+----->
bg714446	+----->
bg393654	+----->
bg704959	+----->
SEQ ID NO 4	+----->
SEQ ID NO 2	+----->
SEQ ID NO 3	+----->

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**Fig. 10: Images of the human cerebral cortex
labeled with anti-hTARPP antiserum and
with DAPI**



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Table 1:

sample	Δ (fold) (frontal / temporal cortex)
patient P012	2.21
patient P016	1.90
patient P010	4.11
patient P011	2.30
patient P014	1.73
patient P017	1.34
patient P019	2.62
control C011	1.24
control C012	1.15
control C014	0.47
control C005	1.39
control C008	1.38

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Table 2:

sample	Δ (fold) (frontal cortex / hippocampus)
<hr/>	
patient P012	1.50
patient P016	3.10
patient P010	5.51
patient P011	2.36
patient P014	1.21
patient P019	1.43
control C005	1.38
control C008	1.10
control C004	1.76